

C. Kaufman

1646

#13

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/878,168A

DATE: 02/23/1999
TIME: 14:30:00

Input Set: H878168A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Ashkenazi, Avi J.
2 Baker, Kevin
3 Gurney, Austin
4 Wood, William
5 <120> TITLE OF INVENTION: Apo-2DcR
6 <130> FILE REFERENCE: 11669.29US02
7 <140> CURRENT APPLICATION NUMBER: US/08/878,168A
8 <141> CURRENT FILING DATE: 1997-06-18
9 <160> NUMBER OF SEQ ID NOS: 17
10 <170> SOFTWARE: FastSEQ for Windows Version 3.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 259
13 <212> TYPE: PRT
14 <213> ORGANISM: HUMAN
15 <400> SEQUENCE: 1
16 Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val Ala
17 1 5 10 15
18 Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu
19 20 25 30
20 Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe
21 35 40 45
22 Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly
23 50 55 60
24 Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
25 65 70 75 80
26 Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
27 85 90 95
28 His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln Cys Lys
29 100 105 110
30 Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys Arg Lys Cys
31 115 120 125
32 Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
33 130 135 140
34 Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu
35 145 150 155 160
36 Thr Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala
37 165 170 175
38 Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro
39 180 185 190
40 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala
41 195 200 205
42 Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
43 210 215 220
44 Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr

Entered

See P.5

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45	225	230	235	240
46	Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile			
47		245	250	255
48	Val Phe Val			
49	<210> SEQ ID NO 2			
50	<211> LENGTH: 1180			
51	<212> TYPE: DNA			
52	<213> ORGANISM: HUMAN			
53	<220> FEATURE:			
54	<221> NAME/KEY: CDS			
55	<222> LOCATION: (193) ... (969)			
56	<400> SEQUENCE: 2			
57	gctgtggaa cctctccacg cgcacgaact cagccaacga tttctgatag attttggaa	60		
58	gtttgaccag agatgcaagg ggtgaaggag cgcttcctac cgtttagggaa ctctggggac	120		
59	agagcgc(ccc) ggccgcctga tggccgaggc agggtgcgac ccaggaccca ggacggcg(c)	180		
60	ggaaaccata cc atg gcc cggtatc ccc aag acc cta aag ttc gtc gtc gtc	231		
61	Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val			
62	1 5 10			
63	atc gtc gcg gtc ctg ctg cca gtc cta gct tac tct gcc acc act gcc	279		
64	Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala			
65	15 20 25			
66	cgg cag gag gaa gtt ccc cag cag aca gtg gcc cca cag caa cag agg	327		
67	Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg			
68	30 35 40 45			
69	cac agc ttc aag ggg gag gag tgt cca gca gga tct cat aga tca gaa	375		
70	His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu			
71	50 55 60			
72	cat act gga gcc tgt aac ccg tgc aca gag ggt gtg gat tac acc aac	423		
73	His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn			
74	65 70 75			
75	gct tcc aac aat gaa cct tct tgc ttc cca tgt aca gtt tgt aaa tca	471		
76	Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser			
77	80 85 90			
78	gat caa aaa cat aaa agt tcc tgc acc atg acc aga gac aca gtg tgt	519		
79	Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys			
80	95 100 105			
81	cag tgt aaa gaa ggc acc ttc cgg aat gaa aac tcc cca gag atg tgc	567		
82	Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys			
83	110 115 120 125			
84	cggttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgt	615		
85	Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn Cys			
86	130 135 140			
87	acgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgttgt	663		
88	Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala			
89	145 150 155			
90	actgt	711		
91	Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly			
92	160 165 170			
93	actcctgcccca gctgctgaa gagacaatg aacaccagc cca ggg act	759		
94	Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr			

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95	175	180	185	
96	cct gcc cca gct gct gaa gag aca atg acc acc agc ccg ggg act cct			807
97	Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro			
98	190	195	200	205
99	gcc cca gct gct gaa gag aca atg acc acc agc ccg ggg act cct gcc			855
100	Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala			
101	210	215	220	
102	cca gct gct gaa gag aca atg acc acc agc ccg ggg act cct gcc tct			903
103	Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser			
104	225	230	235	
105	tct cat tac ctc tca tgc acc atc gta ggg atc ata gtt cta att gtg			951
106	Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val			
107	240	245	250	
108	ctt ctg att gtg ttt gtt tgaaagactt cactgtggaa gaaattccctt			999
109	Leu Leu Ile Val Phe Val			
110	255			
111	ccttacctga aaggttcagg taggcgtgg ctgagggcg ggccgcgtgg acactctctg			1059
112	ccctgcctcc ctctgctgtg ttcccacaga cagaaacgccc tgccccctgcc ccaaaaaaaaa			1119
113	aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa			1179
114	a			1180
115	<210> SEQ ID NO 3			
116	<211> LENGTH: 299			
117	<212> TYPE: PRT			
118	<213> ORGANISM: HUMAN			
119	<400> SEQUENCE: 3			
120	Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp			
121	1	5	10	15
122	Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr			
123	20	25	30	
124	Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu			
125	35	40	45	
126	Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr			
127	50	55	60	
128	Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala			
129	65	70	75	80
130	Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly			
131	85	90	95	
132	Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly			
133	100	105	110	
134	Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys			
135	115	120	125	
136	Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr			
137	130	135	140	
138	Arg Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn			
139	145	150	155	160
140	Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val			
141	165	170	175	
142	Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu			
143	180	185	190	
144	Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met			

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145	195	200	205	
146	Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn			
147	210	215	220	
148	Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr			
149	225	230	235	240
150	Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser			
151	245	250	255	
152	Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro			
153	260	265	270	
154	Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile			
155	275	280	285	
156	Ile Val Leu Ile Val Leu Leu Ile Val Phe Val			
157	290	295		
158	<210> SEQ ID NO 4			
159	<211> LENGTH: 1180			
160	<212> TYPE: DNA			
161	<213> ORGANISM: HUMAN			
162	<220> FEATURE:			
163	<221> NAME/KEY: CDS			
164	<222> LOCATION: (73)...(969)			
165	<221> NAME/KEY: sig_peptide			
166	<222> LOCATION: (73)...(194)			
167	<400> SEQUENCE: 4			
168	gctgtggaa cctctccacg cgcacgaact cagccaacga tttctgatag atttttggga	60		
169	gtttgaccag ag atg caa ggg gtg aag gag cgc ttc cta ccg tta ggg aac		111	
170	Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn			
171	-40	-35	-30	
172	tct ggg gac aga gcg ccc cgg ccg cct gat ggc cga ggc agg gtg cga	159		
173	Ser Gly Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg			
174	-25	-20	-15	
175	ccc agg acc cag gac ggc gtc ggg aac cat acc atg gcc cgg atc ccc	207		
176	Pro Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro			
177	-10	-5	1	5
178	aag acc cta aag ttc gtc gtc atc gtc gcg gtc ctg ctg cca gtc	255		
179	Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val			
180	10	15	20	
181	cta gct tac tct gcc acc act gcc cgg cag gag gaa gtt ccc cag cag	303		
182	Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln			
183	25	30	35	
184	aca gtg gcc cca cag caa cag agg cac agc ttc aag ggg gag gag tgt	351		
185	Thr Val Ala Pro Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys			
186	40	45	50	
187	cca gca gga tct cat aga tca gaa cat act gga gcc tgt aac ccg tgc	399		
188	Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys			
189	55	60	65	
190	aca gag ggt gtg gat tac acc aac gct tcc aac aat gaa cct tct tgc	447		
191	Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys			
192	70	75	80	85
193	ttc cca tgt aca gtt tgt aaa tca gat caa aaa cat aaa agt tcc tgc	495		
194	Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys			

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195	90	95	100	
196	acc atg acc aga gac aca gtg tgt cag tgt aaa gaa ggc acc ttc cgg			543
197	Thr Met Thr Arg Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg			
198	105	110	115	
199	aat gaa aac tcc cca gag atg tgc cgg aag tgt agc agg tgc cct agt			591
200	Asn Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser			
201	120	125	130	
202	ggg gaa gtc caa gtc agt aat tgt acg tcc tgg gat gat atc cag tgt			639
203	Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys			
204	135	140	145	
205	gtt gaa gaa ttt ggt gcc aat gcc act gtg gaa acc cca gct gct gaa			687
206	Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu			
207	150	155	160	165
208	gag aca atg aac acc agc ccg ggg act cct gcc cca gct gct gaa gag			735
209	Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu			
210	170	175	180	
211	aca atg aac acc agc cca ggg act cct gcc cca gct gct gaa gag aca			783
212	Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr			
213	185	190	195	
214	atg acc acc agc ccg ggg act cct gcc cca gct gct gaa gag aca atg			831
215	Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met			
216	200	205	210	
217	acc acc agc ccg ggg act cct gcc cca gct gct gaa gag aca atg acc			879
218	Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr			
219	215	220	225	
220	acc agc ccg ggg act cct gcc tct tct cat tac ctc tca tgc acc atc			927
221	Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile			
222	230	235	240	245
223	gta ggg atc ata gtt cta att gtg ctt ctg att gtg ttt gtt			969
224	Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val			
225	250	255		
226	tgaaaagactt cactgtggaa gaaattcctt ccttacctga aagggtcagg taggcgctgg			1029
227	ctgagggcgg gggcgctgg acactctctg ccctgcctcc ctctgctgtg ttccccacaga			1089
228	cagaaacgcc tgccccgtcc caaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa			1149
229	aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa a			1180
230	<210> SEQ ID NO 5			
231	<211> LENGTH: 43			
232	<212> TYPE: DNA			
233	<213> ORGANISM: YEAST			
234	<400> SEQUENCE: 5			
235	tgtaaaacga cggccagttt aatagacctg caattattaa tct			43
236	<210> SEQ ID NO 6			
237	<211> LENGTH: 41			
238	<212> TYPE: DNA			
239	<213> ORGANISM: YEAST			
240	<400> SEQUENCE: 6			
241	caggaaacag ctatgaccac ctgcacacct gcaaattccat t			41
242	<210> SEQ ID NO 7			
243	<211> LENGTH: 49			
244	<212> TYPE: PRT			

Please Note:

Use 'n' and/or 'Xaa' have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> & <223> fields for each sequence which presents at least one 'n' or 'Xaa'.



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**VERIFICATION SUMMARY
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DATE: 02/23/1999

TIME: 14:30:00

Input Set: H878168A.RAW

Line ? Error/Warning

Original Text

423 W "N" or "Xaa" used: Feature required

Tyr Leu Glu Gly Asn Ala Asp Ser Ala Xaa S